

What is claimed is:

1. An isolated 32374 or 18431 nucleic acid molecule selected from the group consisting of:

5 a) a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number \_\_\_\_\_;

10 b) a nucleic acid molecule comprising a fragment of at least 15 nucleotides of the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number \_\_\_\_\_;

15 c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_;

20 d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_;

25 e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, or a complement thereof, under stringent conditions;

30 f) a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number \_\_\_\_\_; and

g) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_.

2. The isolated nucleic acid molecule of claim 1, which is the nucleotide sequence SEQ ID NO:1 or SEQ ID NO:4.

3. A host cell which contains the nucleic acid molecule of claim 1.

4. An isolated 32374 or 18431 polypeptide selected from the group consisting of:

a) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number \_\_\_\_\_, or a complement thereof;

b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, or a complement thereof under stringent conditions;

c) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2 or SEQ ID NO:5; and

d) the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5.

5. An antibody which selectively binds to a polypeptide of claim 4.

6. A method for producing a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_;

b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_;

c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, SEQ ID NO:5, or the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Accession Number \_\_\_\_\_, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4 or SEQ ID NO:6; and

d) the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5; comprising culturing the host cell of claim 3 under conditions in which the nucleic acid molecule is expressed.

7. A method for detecting the presence of a nucleic acid molecule of claim 1 or a polypeptide encoded by the nucleic acid molecule in a sample, comprising:

a) contacting the sample with a compound which selectively hybridizes to the nucleic acid molecule of claim 1 or binds to the polypeptide encoded by the nucleic acid molecule; and

b) determining whether the compound hybridizes to the nucleic acid or binds to the polypeptide in the sample.

8. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 or binds to a polypeptide encoded by the nucleic acid molecule and instructions for use.

9. A method for identifying a compound which binds to a polypeptide or modulates the activity of the polypeptide of claim 4 comprising the steps of:

- a) contacting a polypeptide, or a cell expressing a polypeptide of claim 4 with a test compound; and
- b) determining whether the polypeptide binds to the test compound or determining the effect of the test compound on the activity of the polypeptide.

10. A method for modulating the activity of a polypeptide of claim 4 comprising contacting the polypeptide or a cell expressing the polypeptide with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

11. A method of identifying a nucleic acid molecule associated with a disorder comprising:

- a) contacting a sample from a subject with or at risk of developing a disorder comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or SEQ ID NO:4 defined in claim 2; and
- b) detecting the presence of a nucleic acid molecule in the sample that hybridizes to the probe, thereby identifying a nucleic acid molecule associated with a disorder.

12. A method of identifying a nucleic acid associated with a disorder comprising:

- a) contacting a sample from a subject having a disorder or at risk of developing a disorder comprising nucleic acid molecules with a first and a second amplification primer, the first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or SEQ ID NO:4 defined in claim 2 and the second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1 or SEQ ID NO:4;

b) incubating the sample under conditions that allow nucleic acid amplification; and

- c) detecting the presence of a nucleic acid molecule in the sample that is amplified, thereby identifying the nucleic acid molecule associated with a disorder.

13. A method of identifying a polypeptide associated with a disorder comprising:

a) contacting a sample comprising polypeptides with a 32374 or 18431 binding partner of the 32374 or 18431 polypeptide defined in claim 4; and

b) detecting the presence of a polypeptide in the sample that binds to the 32374 or 18431 binding partner, thereby identifying the polypeptide associated with a disorder.

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14. A method of identifying a subject having a disorder or at risk for developing a disorder comprising:

a) contacting a sample obtained from the subject comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or SEQ ID NO:4 defined in claim 2; and

b) detecting the presence of a nucleic acid molecule in the sample that hybridizes to the probe, thereby identifying a subject having a disorder or at risk for developing a disorder.

15. A method of identifying a subject having a disorder or at risk for developing a disorder comprising:

a) contacting a sample obtained from the subject comprising nucleic acid molecules with a first and a second amplification primer, the first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or SEQ ID NO:4 defined in claim 2 and the second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1 or SEQ ID NO:4;

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b) incubating the sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in the sample that is amplified, thereby identifying a subject having a disorder or at risk for developing a disorder.

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16. A method of identifying a subject having a disorder or at risk for developing a disorder comprising:

a) contacting a sample obtained from the subject comprising polypeptides with a 32374 or 18431 binding partner of the 32374 or 18431 polypeptide defined in claim 4; and

b) detecting the presence of a polypeptide in the sample that binds to the 32374 or 18431 binding partner, thereby identifying a subject having a disorder or at risk for developing a disorder.

17. A method for identifying a compound capable of treating a disorder characterized by aberrant 32374 or 18431 nucleic acid expression or 32374 or 18431 polypeptide activity comprising assaying the ability of the compound to modulate 32374 or 18431 nucleic acid expression or 32374 or 18431 polypeptide activity, thereby identifying a compound capable of treating a disorder characterized by aberrant 32374 or 18431 nucleic acid expression or 32374 or 18431 polypeptide activity.

18. A method for treating a subject having a disorder or at risk of developing a disorder comprising administering to the subject a 32374 or 18431 modulator of the nucleic acid molecule defined in claim 1 or the polypeptide encoded by the nucleic acid molecule or contacting a cell with a 32374 or 18431 modulator.

19. The method of claim 18, wherein the 32374 or 18431 modulator is

- a) a small molecule;
- b) peptide;
- c) phosphopeptide;
- d) anti-32374 or 18431 antibody;
- e) a 32374 or 18431 polypeptide comprising the amino acid sequence of SEQ ID

NO:2, SEQ ID NO:5, or a fragment thereof;

f) a 32374 or 18431 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5, wherein the percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4; or

g) an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid

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molecule consisting of SEQ ID NO:1 or SEQ ID NO:4 at 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C.

20. The method of claim 18, wherein the 32374 or 18431 modulator is

a) an antisense 32374 or 18431 nucleic acid molecule;

b) is a ribozyme;

c) the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:4, or a fragment thereof;

d) a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5, wherein the percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4;

e) a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or SEQ ID NO:4 at 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C; or

f) a gene therapy vector.

21. A method for evaluating the efficacy of a treatment of a disorder, in a subject, comprising:

treating a subject with a protocol under evaluation;

assessing the expression level of a 32374 or 18431 nucleic acid molecule defined in claim 1 or 32374 or 18431 polypeptide encoded by the 32374 or 18431 nucleic acid molecule,

wherein a change in the expression level of 32374 or 18431 nucleic acid or 32374 or 18431 polypeptide after the treatment, relative to the level before the treatment, is indicative of the efficacy of the treatment of a disorder.

22. A method of diagnosing a disorder in a subject, comprising:

evaluating the expression or activity of a 32374 or 18431 nucleic acid molecule defined in claim 1 or a 32374 or 18431 polypeptide encoded by the 32374 or 18431 nucleic acid molecule, such that a difference in the level of 32374 or 18431 nucleic acid or 32374 or 18431 polypeptide relative to a normal subject or a cohort of normal subjects is indicative of a disorder.

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23. The method defined in claim 18, wherein the disorder is cancer or aberrant cellular proliferation and/or differentiation, a pain or metabolic disorder, or a brain disorder.

24. The method defined in claim 23, wherein the cancer or aberrant cellular proliferation and/or differentiation is lung, ovarian, or brain cancer.

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